Please amend claims 1-12, add new claims 13-15 as follows:

1.   (Currently Amended) A method for assembling nucleic acid base sequences comprising the steps of:

providing a plurality of nucleic acid base sequences;

moving a window of <u>a</u> fixed length along a first nucleic acid base sequence <u>of the plurality of nucleic acid base sequences to define a first fixed-length partial sequence</u> and simultaneously searching for a second nucleic acid base sequence <u>among the plurality of nucleic acid base sequences</u> which has a <u>second fixed-length</u> partial sequence at a terminal region thereof <u>exactly</u> matching with <u>the first fixed-length partial</u> sequence defined by the window;

determining whether the second nucleic acid base sequence searched in said <u>moving</u> step and the first nucleic acid base sequence can be assembled or not <u>by comparing a sequence adjacent to said first fixed-length partial sequence of said first nucleic acid base sequence with a sequence adjacent to said second fixed-length partial sequence of the second nucleic acid base sequence to be sufficiently similar via a greedy alignment algorithm</u>; and

assembling said first nucleic acid base sequence and said second nucleic acid bases sequence if <s>said step determines that</s> the second nucleic acid base sequence and the first nucleic acid base sequence <s>can</s> <u>are determined to</u> be assembled.

2.   (Currently Amended) A method for assembling nucleic acid base sequences <u>according to claim 1,</u> <s>comprising the steps of:</s>

<s>moving a window of fixed length along a first nucleic acid base sequence and simultaneously searching for a second nucleic acid base sequence which has a partial sequence at a terminal region thereof matching with a sequence defined by the window;</s>

<s>determining whether the second nucleic acid base sequence searched in said step and the first nucleic acid base sequence can be assembled or not; and</s>

<s>assembling said first nucleic acid base sequence and said second nucleic acid base sequence if said step determines that the second nucleic acid base sequence and the first</s>

~~nucleic acid base sequence can be assembled,~~

wherein the nucleic acid base sequence assembled in said <u>assembling</u> step is used as a [[new]] **reconstructed** first nucleic acid base sequence to repeatedly carry out said <u>moving, determining, and assembling</u> steps.

3. (Currently Amended) A method for assembling nucleic acid sequences comprising the steps of:

<u>providing a plurality of nucleic acid base sequences;</u>

entering identification information [[about]] <u>of</u> each of [[a]] <u>the</u> plurality of nucleic acid base sequences and a <u>respective</u> fixed-length partial sequence located in a terminal region of <u>each of</u> the nucleic acid base sequence<u>s</u> into a table~~, both of which are associated with each other~~;

constructing a first consensus sequence based on a first nucleic acid base sequence <u>of the plurality of nucleic acid base sequences</u>;

searching for a <u>second</u> nucleic acid base sequence <u>among remaining ones of the plurality of nucleic acid base sequences</u> which has a <u>second fixed-length</u> partial sequence <u>exactly</u> matching with a [[part]] <u>first partial sequence</u> of said <u>first</u> consensus sequence with reference to said table;

comparing a sequence adjacent to said <u>second fixed-length</u> partial sequence of the <u>second</u> nucleic acid base sequence searched in said <u>searching</u> step with a sequence adjacent to said <u>first fixed-length</u> partial sequence of said <u>first</u> consensus sequence <u>to be sufficiently similar via a greedy alignment algorithm</u> [[, and]] <u>thereby</u> determining ~~whether~~ the ~~searched~~ <u>second</u> nucleic acid base sequence can be assembled to said <u>first</u> consensus sequence ~~or not~~; and

assembling said <u>second</u> nucleic acid base sequence to said <u>first</u> consensus sequence so as to reconstruct a **reconstructed** <u>first</u> consensus sequence if ~~said step determines that~~ the <u>second</u> nucleic acid base sequence ~~can~~ <u>is determined to</u> be assembled to the <u>first</u> consensus sequence.

4. (Currently Amended) The method for assembling nucleic acid base sequences according to claim 3, wherein a sequence whose base length is the longest among ~~unprocessed~~ <u>the plurality of</u> nucleic acid base sequences is selected as said first nucleic acid base

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sequence.

5. (Currently Amended) A method for assembling nucleic acid base sequences comprising:

a first step of sorting a plurality of nucleic acid base sequences in descending order of ~~their~~ sequence lengths;

a second step of entering identification information [[about]] of each of the plurality of nucleic acid base sequences and a respective pair of fixed-length partial sequences located in ~~the head end and tail end regions~~ a terminal region thereof ~~input nucleic acid base sequences~~ into a table~~, both of which are associated with each other~~;

a third step of selecting one of the nucleic acid base sequences whose sequence length is the longest among the plurality of ~~unprocessed~~ nucleic acid base sequences~~, and constructing~~ as a first consensus sequence;

a fourth step of moving a fixed length window along said first consensus sequence to define a first fixed-length partial sequence and simultaneously searching for ~~an unprocessed~~ a second nucleic acid base sequence among remaining ones of the plurality of nucleic acid base sequences which has a second fixed-length partial sequence exactly matching with [[a]] the first fixed-length partial sequence defined by said fixed length window with reference to said table;

a fifth step of comparing a sequence adjacent to said first fixed-length partial sequence of said first consensus sequence with a sequence adjacent to said second fixed-length partial sequence of the ~~unprocessed~~ second nucleic acid base sequence searched in said fourth step to be sufficiently similar via a greedy alignment algorithm [[, and]] thereby determining ~~whether~~ said first consensus sequence and the ~~both sequences~~ second nucleic acid base sequence to ~~can~~ be assembled ~~or not~~; and

a sixth step of assembling the second nucleic acid base sequence searched in said fourth step to said first consensus sequence so as to reconstruct a **reconstructed** first consensus sequence if said fifth step determines that the ~~both~~ sequences ~~can~~ are to be assembled,

wherein the fourth step to the sixth step are repeated until said fixed length window completes the scanning throughout said **reconstructed** first consensus sequence, and said third step to said sixth step are repeated ~~if any unprocessed~~ until all of the plurality of nucleic acid base sequences are selected in the fourth step and compared in

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the fifth step ~~still remains~~.

6.   (Currently Amended) The method for assembling nucleic acid base sequences according to claim 3, further comprising a step of specifying a number of said ~~fixed base~~ fixed-length ~~of~~ partial sequences to be entered into said table for ~~one~~ each of the plurality of nucleic acid base sequences.

7.   (Currently Amended) The method for assembling nucleic acid base sequences according to claim 3, further comprising a step of designating a range of the terminal region ~~head end and tail end regions~~ of said first nucleic acid base sequence from which said fixed-length partial sequences to be entered into said table is extracted.

8.   (Currently Amended) The method for assembling nucleic acid base sequences according to claim 3, wherein a base length of said ~~fixed base~~ fixed-length ~~of~~ partial sequences to be entered into said table is between ~~at least~~ 10 bases ~~or more~~ and 32 bases ~~or less~~.

9.   (Currently Amended) The method for assembling nucleic acid base sequences according to claim 3, further comprising:

a step of specifying an upper limit c ~~on the~~ as an expected ~~value of the~~ number of entries ~~which are detected upon once making reference to~~ retrieved from said table of an identical fixed-length partial sequence located in different nucleic acid base sequences or different positions in the nucleic acid base ~~and their associated input~~ sequences ~~are determined not to be able~~ to be assembled to said first consensus sequences, and

a step of specifying [[the]] a length s of fixed-length partial sequences to be entered into said table as an integer satisfying the following expression (1)

$$s \geq \frac{1}{2} \log \frac{KN}{c} \quad \cdots (1)$$

where N is the number of said plurality of [[input]] nucleic acid base sequences and K is the number of the fixed-length partial sequences selected from each of the plurality of nucleic acid base sequences.

10..   (Currently Amended) The method for assembling nucleic acid base sequences according

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to claim 13, wherein a 3'-end region or a 5'-end region of said first nucleic acid base sequence are simultaneously entered into the table to proceed the searching, comparing, and assembling steps ~~two-way lists are used to implement said consensus sequences~~.

11.   (Currently Amended) The method for assembling nucleic acid base sequences according to claim 3, wherein [[a]] each of said ~~fixed-base~~ fixed-length ~~of~~ partial sequence<u>s</u> is represented by a fixed number of computing words which are independent of [[the]] <u>a</u> length of the fixed-length partial sequences.

12.   (Currently Amended) The method for assembling nucleic acid base sequences according to claim 3, wherein only entries <u>in said table</u> corresponding to a key, which <u>is the</u> <u>frequency of occurrence of said second fixed-length partial sequence</u> ~~occurs a previously specified number of times or less~~ in said table, are utilized <u>as said second fixed-length</u> <u>partial sequence for searching for said second nucleic acid base sequence</u>.

13.   (New) The method for assembling nucleic acid base sequences according to claim 3, wherein a respective pair of fixed-length partial sequences in the 3'-end region and the 5'-end region said first nucleic acid base sequence.

14.   (New) The method for assembling nucleic acid base sequences according to claim 9, wherein c satisfies $NK/4^s \leq c$.

15.   (New) The method for assembling nucleic acid base sequences according to claim 9, wherein N= 65536, K=2, and s=10.